RAW SEQUENCE LISTING

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Application Serial Number: __10/556,221__

Source: __IFWP__

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IFWP

RAW SEQUENCE LISTING   DATE: 12/08/2006
PATENT APPLICATION: US/10/556,221   TIME: 09:06:01

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Output Set: **N:\CRF4\12082006\J556221.raw**

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 3 <110> APPLICANT: Universite Laval
 4       De Koninck, Yves
 5       De Koninck, Paul
 6       Coull, Jeffrey
 8 <120> TITLE OF INVENTION: CNS chloride modulation and uses thereof
10 <130> FILE REFERENCE: 85409-29
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C--> 12 <140> **CURRENT APPLICATION NUMBER: US/10/556,221**
C--> 12 <141> **CURRENT FILING DATE: 2005-11-09**
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12 <150> PRIOR APPLICATION NUMBER: US 60/470,885
13 <151> PRIOR FILING DATE: 2003-05-16
15 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 5907
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(3351)
29 <400> SEQUENCE: 1
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32 1               5                   10                  15
34 ccg ggt gat ggc aac ccc aag gaa agc agt ccc ttc atc aac agc acc      96
35 Pro Gly Asp Gly Asn Pro Lys Glu Ser Ser Pro Phe Ile Asn Ser Thr
36             20                  25                  30
38 gac aca gag aag gga aag gag tat gat ggc aag aac atg gcc ttg ttt     144
39 Asp Thr Glu Lys Gly Lys Glu Tyr Asp Gly Lys Asn Met Ala Leu Phe
40         35                  40                  45
42 gag gag gag atg gac acc agc cct atg gtg tcc tcc ttg ctc agt ggc     192
43 Glu Glu Glu Met Asp Thr Ser Pro Met Val Ser Ser Leu Leu Ser Gly
44      50                  55                  60
46 ctg gcc aac tac acc aac ctg ccc cag gga agt agg gag cat gaa gag     240
47 Leu Ala Asn Tyr Thr Asn Leu Pro Gln Gly Ser Arg Glu His Glu Glu
48 65                  70                  75                  80
50 gca gaa aac aat gag ggt gga aaa aag aag ccg gtg cag gcc cca cgc     288
51 Ala Glu Asn Asn Glu Gly Gly Lys Lys Lys Pro Val Gln Ala Pro Arg
52                  85                  90                  95
54 atg ggc acc ttc atg ggc gtg tac ctg ccg tgc ctg cag aac atc ttt     336
55 Met Gly Thr Phe Met Gly Val Tyr Leu Pro Cys Leu Gln Asn Ile Phe
56             100                 105                 110
58 ggc gtc atc ctc ttc ctg cgg ctc acc tgg gtg gtg ggc att gca ggc     384
59 Gly Val Ile Leu Phe Leu Arg Leu Thr Trp Val Val Gly Ile Ala Gly
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60         115               120               125
62 atc atg gag tcc ttc tgc atg gtg ttc atc tgc tgc tcc tgt acg atg       432
63 Ile Met Glu Ser Phe Cys Met Val Phe Ile Cys Cys Ser Cys Thr Met
64     130               135               140
66 ctc acg gcc atc tcc atg agt gca att gca acg aat ggt gtt gtg cct       480
67 Leu Thr Ala Ile Ser Met Ser Ala Ile Ala Thr Asn Gly Val Val Pro
68 145               150               155               160
70 gct ggt ggc tcc tac tac atg att tcc agg tct ctg ggc cca gag ttt       528
71 Ala Gly Gly Ser Tyr Tyr Met Ile Ser Arg Ser Leu Gly Pro Glu Phe
72               165               170               175
74 ggg ggt gcc gtg ggc ctc tgc ttc tac ctg ggc act acc ttt gca gga       576
75 Gly Gly Ala Val Gly Leu Cys Phe Tyr Leu Gly Thr Thr Phe Ala Gly
76               180               185               190  .
78 gcc atg tac atc ctg ggc acc atc gaa atc ctg ctg gct tac ctc ttc       624
79 Ala Met Tyr Ile Leu Gly Thr Ile Glu Ile Leu Leu Ala Tyr Leu Phe
80         195               200               205
82 cca gcc atg gcc atc ttc aag gca gaa gat gcc agt ggg gag gca gca       672
83 Pro Ala Met Ala Ile Phe Lys Ala Glu Asp Ala Ser Gly Glu Ala Ala
84     210               215               220
86 gcc atg ctg aac aac atg cgt gtt tac ggc acc tgt gtg ctc acc tgc       720
87 Ala Met Leu Asn Asn Met Arg Val Tyr Gly Thr Cys Val Leu Thr Cys
88 225               230               235               240
90 atg gcc act gtg gtg ttt gtg ggt gtc aag tat gtc aac aag ttt gcc       768
91 Met Ala Thr Val Val Phe Val Gly Val Lys Tyr Val Asn Lys Phe Ala
92               245               250               255
94 ctt gtc ttc ctg ggt tgt gtc atc ctc tcc atc ctg gcc atc tat gct       816
95 Leu Val Phe Leu Gly Cys Val Ile Leu Ser Ile Leu Ala Ile Tyr Ala
96               260               265               270
98 ggg gtc atc aag tct gcc ttc gac cca ccc aac ttc ccg atc tgc ctc       864
99 Gly Val Ile Lys Ser Ala Phe Asp Pro Pro Asn Phe Pro Ile Cys Leu
100         275               280               285
102 ctg ggt aac cgc acg ctg tct cgc cat ggc ttt gat gtc tgt gcc aag      912
103 Leu Gly Asn Arg Thr Leu Ser Arg His Gly Phe Asp Val Cys Ala Lys
104     290               295               300
106 ctg gct tgg gaa gga aat gag acg gtg acc aca cgg cta tgg ggc ctt      960
107 Leu Ala Trp Glu Gly Asn Glu Thr Val Thr Thr Arg Leu Trp Gly Leu
108 305               310               315               320
110 ttc tgc tcc tct cgc ttc ctc aac gcc acc tgt gat gaa tac ttc acc      1008
111 Phe Cys Ser Ser Arg Phe Leu Asn Ala Thr Cys Asp Glu Tyr Phe Thr
112               325               330               335
114 cga aac aat gtc aca gag atc cag ggc atc cct ggt gct gcc agt ggc      1056
115 Arg Asn Asn Val Thr Glu Ile Gln Gly Ile Pro Gly Ala Ala Ser Gly
116               340               345               350
118 ctc atc aaa gag aac ctc tgg agc tcc tac ctg acc aag ggc gtg att      1104
119 Leu Ile Lys Glu Asn Leu Trp Ser Ser Tyr Leu Thr Lys Gly Val Ile
120         355               360               365
122 gtg gag agg agt ggg atg acc tcg gtg ggc ctg gcc gat ggc act cct      1152
123 Val Glu Arg Ser Gly Met Thr Ser Val Gly Leu Ala Asp Gly Thr Pro
124     370               375               380
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126 atc gac atg gac cac cct tat gtc ttc agt gat atg acc tcc tac ttc    1200
127 Ile Asp Met Asp His Pro Tyr Val Phe Ser Asp Met Thr Ser Tyr Phe
128 385                 390                 395                 400
130 acc ctg ctg gtt ggc atc tac ttc ccc tca gtc aca ggg atc atg gct    1248
131 Thr Leu Leu Val Gly Ile Tyr Phe Pro Ser Val Thr Gly Ile Met Ala
132             405                 410                 415
134 ggt tct aac cgc tct ggg gac ctg agg gat gcc cag aag tca atc ccc    1296
135 Gly Ser Asn Arg Ser Gly Asp Leu Arg Asp Ala Gln Lys Ser Ile Pro
136             420                 425                 430
138 act ggc acc atc ctg gcc atc gcc acc acc tct gct gtc tac atc agc    1344
139 Thr Gly Thr Ile Leu Ala Ile Ala Thr Thr Ser Ala Val Tyr Ile Ser
140             435                 440                 445
142 tcc gtt gtt ctg ttt ggg gcc tgc att gag ggg gtc gtc ctg cgg gac    1392
143 Ser Val Val Leu Phe Gly Ala Cys Ile Glu Gly Val Val Leu Arg Asp
144     450                 455                 460
146 aag ttt ggc gaa gct gtg aat ggc aac ctc gtg gtg ggc act ctg gcc    1440
147 Lys Phe Gly Glu Ala Val Asn Gly Asn Leu Val Val Gly Thr Leu Ala
148 465                 470                 475                 480
150 tgg cca tct cca tgg gta att gtc atc gga tcc ttc ttc tcc acc tgt    1488
151 Trp Pro Ser Pro Trp Val Ile Val Ile Gly Ser Phe Phe Ser Thr Cys
152             485                 490                 495
154 ggg gct ggg ctg cag agc ctc acg ggg gcc cca cgc ctg ctg cag gcc    1536
155 Gly Ala Gly Leu Gln Ser Leu Thr Gly Ala Pro Arg Leu Leu Gln Ala
156             500                 505                 510
158 atc tcg agg gat ggc att gtg ccc ttc ctg cag gtc ttt ggc cat ggc    1584
159 Ile Ser Arg Asp Gly Ile Val Pro Phe Leu Gln Val Phe Gly His Gly
160         515                 520                 525
162 aag gcc aat gga gag ccg acc tgg gcc ctg ctc ctg act gcc tgc atc    1632
163 Lys Ala Asn Gly Glu Pro Thr Trp Ala Leu Leu Leu Thr Ala Cys Ile
164     530                 535                 540
166 tgc gag att ggc atc ctc att gca tcc ctc gac gag gtg gcc ccc atc    1680
167 Cys Glu Ile Gly Ile Leu Ile Ala Ser Leu Asp Glu Val Ala Pro Ile
168 545                 550                 555                 560
170 ctc tct atg ttc ttc ctg atg tgc tac atg ttt gtg aat ctg gcc tgt    1728
171 Leu Ser Met Phe Phe Leu Met Cys Tyr Met Phe Val Asn Leu Ala Cys
172             565                 570                 575
174 gca gtg cag acg ctg ctg agg aca ccc aac tgg agg cca cgc ttt cga    1776
175 Ala Val Gln Thr Leu Leu Arg Thr Pro Asn Trp Arg Pro Arg Phe Arg
176             580                 585                 590
178 tat tac cac tgg acc ctc tcc ttc ctg ggc atg agc ctc tgc ctg gcc    1824
179 Tyr Tyr His Trp Thr Leu Ser Phe Leu Gly Met Ser Leu Cys Leu Ala
180         595                 600                 605
182 ctc atg ttc atc tgc tcc tgg tat tat gca ctg gta gcc atg ctc att    1872
183 Leu Met Phe Ile Cys Ser Trp Tyr Tyr Ala Leu Val Ala Met Leu Ile
184     610                 615                 620
186 gct gga ctc atc tac aag tac att gag tac cgt ggg gca gag aag gag    1920
187 Ala Gly Leu Ile Tyr Lys Tyr Ile Glu Tyr Arg Gly Ala Glu Lys Glu
188 625                 630                 635                 640
190 tgg ggc gat ggg ata cga ggt ctg tct ctc agt gcg gct cgc tat gcc    1968
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191 Trp Gly Asp Gly Ile Arg Gly Leu Ser Leu Ser Ala Ala Arg Tyr Ala
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194 ctc tta cgc ctg gag gaa ggg ccc cca cac acc aag aac tgg agg cca      2016
195 Leu Leu Arg Leu Glu Glu Gly Pro Pro His Thr Lys Asn Trp Arg Pro
196             660             665             670
198 cag ctg ctg gtg ctg gtg cgt gtg gac caa gac cag aat gtg gtg cac      2064
199 Gln Leu Leu Val Leu Val Arg Val Asp Gln Asp Gln Asn Val Val His
200             675             680             685
202 ccc cag ctg ctc tca ctg acc tcc cag ctg aag gca ggg aag ggc ctg      2112
203 Pro Gln Leu Leu Ser Leu Thr Ser Gln Leu Lys Ala Gly Lys Gly Leu
204             690             695             700
206 acc atc gtg ggc tct gtc ctt gag ggc acc ttt ctg gaa aat cat cca      2160
207 Thr Ile Val Gly Ser Val Leu Glu Gly Thr Phe Leu Glu Asn His Pro
208 705             710             715             720
210 cag gcc cag cgg gca gaa gag tct atc agg cgc ctg atg gag gca gag      2208
211 Gln Ala Gln Arg Ala Glu Glu Ser Ile Arg Arg Leu Met Glu Ala Glu
212             725             730             735
214 aag gtg aag ggc ttc tgc cag gtg gtg atc tcc tcc aac ttg cgt gat      2256
215 Lys Val Lys Gly Phe Cys Gln Val Val Ile Ser Ser Asn Leu Arg Asp
216             740             745             750
218 ggc gtg tcc cat ctg atc cag tcc ggg ggc ctc ggg ggg ctg cag cac      2304
219 Gly Val Ser His Leu Ile Gln Ser Gly Gly Leu Gly Gly Leu Gln His
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222 aac act gtg ctt gtt ggc tgg ccc cgc aac tgg cgc cag aag gaa gat      2352
223 Asn Thr Val Leu Val Gly Trp Pro Arg Asn Trp Arg Gln Lys Glu Asp
224             770             775             780
226 cat cag acg tgg agg aac ttc att gag ctg gtc cgg gaa acc aca gct      2400
227 His Gln Thr Trp Arg Asn Phe Ile Glu Leu Val Arg Glu Thr Thr Ala
228 785             790             795             800
230 ggc cac tta gcc ctg ctg gtc acc aag aac gtt tcc atg ttt cct ggg      2448
231 Gly His Leu Ala Leu Leu Val Thr Lys Asn Val Ser Met Phe Pro Gly
232             805             810             815
234 aac cct gag cgc ttc tct gag ggc agc atc gac gtt tgg tgg att gtg      2496
235 Asn Pro Glu Arg Phe Ser Glu Gly Ser Ile Asp Val Trp Trp Ile Val
236             820             825             830
238 cac gat gga ggc atg ctc atg ctg ctg ccc ttc ctg ctg cgg cac cac      2544
239 His Asp Gly Gly Met Leu Met Leu Leu Pro Phe Leu Leu Arg His His
240             835             840             845
242 aag gtc tgg cgg aag tgc aag atg cgt atc ttc act gtg gcc cag atg      2592
243 Lys Val Trp Arg Lys Cys Lys Met Arg Ile Phe Thr Val Ala Gln Met
244     850             855             860
246 gat gac aat agc atc cag atg aag aag gat ctg acc aca ttt ctg tat      2640
247 Asp Asp Asn Ser Ile Gln Met Lys Lys Asp Leu Thr Thr Phe Leu Tyr
248 865             870             875             880
250 cat tta cgc atc act gcg gag gtc gag gtg gtg gag atg cat gag agc      2688
251 His Leu Arg Ile Thr Ala Glu Val Glu Val Val Glu Met His Glu Ser
252             885             890             895
254 gac atc tca gct tac acc tat gag aag acg ttg gtg atg gag cag cgt      2736
255 Asp Ile Ser Ala Tyr Thr Tyr Glu Lys Thr Leu Val Met Glu Gln Arg
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256          900              905              910
258 tcc cag atc ctc aaa cag atg cat tta acc aag aat gag cgg gag cgg    2784
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260          915              920              925
262 gag atc cag agt atc aca gat gag tca cga ggc tca atc cgg aga aag    2832
263 Glu Ile Gln Ser Ile Thr Asp Glu Ser Arg Gly Ser Ile Arg Arg Lys
264          930              935              940
266 aat cca gcc aac acg cgg ctc cgc ctg aac gtc cca gaa gag acg gct    2880
267 Asn Pro Ala Asn Thr Arg Leu Arg Leu Asn Val Pro Glu Glu Thr Ala
268 945              950              955              960
270 ggt gac agt gaa gag aag cca gag gag gag gtg cag ctg atc cac gat    2928
271 Gly Asp Ser Glu Glu Lys Pro Glu Glu Glu Val Gln Leu Ile His Asp
272              965              970              975
274 cag agt gct ccc agc tgc ccc agc agc tcc ccg tcc cca ggg gag gag    2976
275 Gln Ser Ala Pro Ser Cys Pro Ser Ser Ser Pro Ser Pro Gly Glu Glu
276          980              985              990
278 cct gag ggg gaa ggg gag aca gat  ccg gag aag gtg cat  ctc acc tgg   3024
279 Pro Glu Gly Glu Gly Glu Thr Asp  Pro Glu Lys Val His  Leu Thr Trp
280          995              1000             1005
282 acc aag  gac aag tcg gtg gca  gag aag aat aag ggc  ccc agt cct     3069
283 Thr Lys  Asp Lys Ser Val Ala  Glu Lys Asn Lys Gly  Pro Ser Pro
284      1010             1015             1020
286 gtc tcc  tct gag ggc atc aag  gac ttc ttc agc atg  aag ccg gag     3114
287 Val Ser  Ser Glu Gly Ile Lys  Asp Phe Phe Ser Met  Lys Pro Glu
288      1025             1030             1035
290 tgg gag  aac ttg aac cag tcc  aac gtg cgg cgc atg  cac acg gcc     3159
291 Trp Glu  Asn Leu Asn Gln Ser  Asn Val Arg Arg Met  His Thr Ala
292      1040             1045             1050
294 gtg cgg  ctg aac gag gtc atc  gtg aag aaa tcc cgg  gac gcc aag     3204
295 Val Arg  Leu Asn Glu Val Ile  Val Lys Lys Ser Arg  Asp Ala Lys
296      1055             1060             1065
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299 Leu Val  Leu Leu Asn Met Pro  Gly Pro Pro Arg Asn  Arg Asn Gly
300      1070             1075             1080
302 gat gaa  aac tac atg gag ttt  ctc gag gtc ctc aca  gag cac ctg     3294
303 Asp Glu  Asn Tyr Met Glu Phe  Leu Glu Val Leu Thr  Glu His Leu
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306 gac cgg  gtg atg ctg gtc cgc  ggt ggt ggc cga gag  gtc atc acc     3339
307 Asp Arg  Val Met Leu Val Arg  Gly Gly Gly Arg Glu  Val Ile Thr
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310 atc tac  tcc tga gaaccaggtc ctgccacccg ggcccgagcg cgcccggccc       3391
311 Ile Tyr  Ser
312      1115
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318 gattcggaga gggcgccccg ccgcgcagag accagagctc ctcagtgcca gtttggcccc    3571
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322 aaaggttggg agaaggcgcg gaaaggagag gagctggggc cttggggacc cccaggtagt    3691
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VERIFICATION SUMMARY DATE: 12/08/2006
PATENT APPLICATION: **US/10/556,221** TIME: 09:06:02

Input Set : **A:\PTO.RJ.txt**
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date